RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/757,077B

Source: TFW 16

Date Processed by STIC: 2/5/07

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 02/05/2007
PATENT APPLICATION: **US/10/757,077B**   TIME: 14:53:27

Input Set : **A:\17355CIP3SEQLIST.TXT**
Output Set: **N:\CRF4\02052007\J757077B.raw**

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 4 <110> APPLICANT: Steward, Lance E.
 5        Fernandez-Salas, Ester
 6        Herrington, Todd
 7        Aoki, Kei Roger
 9 <120> TITLE OF INVENTION: Clostridial Neurotoxin Compositions and
10        Modified Clostridial Neurotoxins
13 <130> FILE REFERENCE: 17355CIP3 (BOT)
15 <140> CURRENT APPLICATION NUMBER: US 10/757,077B
16 <141> CURRENT FILING DATE: 2004-01-14
18 <150> PRIOR APPLICATION NUMBER: US 09/910,346
19 <151> PRIOR FILING DATE: 2001-07-20
21 <150> PRIOR APPLICATION NUMBER: US 09/620,840
22 <151> PRIOR FILING DATE: 2000-07-21
24 <150> PRIOR APPLICATION NUMBER: US 10/163,106
25 <151> PRIOR FILING DATE: 2003-06-04
27 <160> NUMBER OF SEQ ID NOS: 83
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 7
33 <212> TYPE: PRT
34 <213> ORGANISM: Clostridium botulinum serotype A
36 <400> SEQUENCE: 1
37 Phe Glu Phe Tyr Lys Leu Leu
38 1               5
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 7
43 <212> TYPE: PRT
44 <213> ORGANISM: Rattus norvegicus
46 <400> SEQUENCE: 2
47 Glu Glu Lys Arg Ala Ile Leu
48 1               5
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 7
53 <212> TYPE: PRT
54 <213> ORGANISM: Rattus norvegicus
56 <400> SEQUENCE: 3
57 Glu Glu Lys Met Ala Ile Leu
58 1               5
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 7
63 <212> TYPE: PRT
64 <213> ORGANISM: Rattus norvegicus
66 <400> SEQUENCE: 4
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 67 Ser Glu Arg Asp Val Leu Leu
 68  1               5
 71 <210> SEQ ID NO: 5
 72 <211> LENGTH: 7
 73 <212> TYPE: PRT
 74 <213> ORGANISM: Rattus norvegicus
 76 <400> SEQUENCE: 5
 77 Val Asp Thr Gln Val Leu Leu
 78  1               5
 81 <210> SEQ ID NO: 6
 82 <211> LENGTH: 7
 83 <212> TYPE: PRT
 84 <213> ORGANISM: Mus musculus
 86 <400> SEQUENCE: 6
 87 Ala Glu Val Gln Ala Leu Leu
 88  1               5
 91 <210> SEQ ID NO: 7
 92 <211> LENGTH: 7
 93 <212> TYPE: PRT
 94 <213> ORGANISM: Xenopus laevis
 96 <400> SEQUENCE: 7
 97 Ser Asp Lys Gln Asn Leu Leu
 98  1               5
101 <210> SEQ ID NO: 8
102 <211> LENGTH: 7
103 <212> TYPE: PRT
104 <213> ORGANISM: Gallus gallus
106 <400> SEQUENCE: 8
107 Ser Asp Arg Gln Asn Leu Ile
108  1               5
111 <210> SEQ ID NO: 9
112 <211> LENGTH: 7
113 <212> TYPE: PRT
114 <213> ORGANISM: Ovis aries
116 <400> SEQUENCE: 9
117 Ala Asp Thr Gln Val Leu Met
118  1               5
121 <210> SEQ ID NO: 10
122 <211> LENGTH: 7
123 <212> TYPE: PRT
124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 10
127 Ser Asp Lys Asn Thr Leu Leu
128  1               5
131 <210> SEQ ID NO: 11
132 <211> LENGTH: 7
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 11
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137 Ser Gln Ile Lys Arg Leu Leu
138  1               5
141 <210> SEQ ID NO: 12
142 <211> LENGTH: 7
143 <212> TYPE: PRT
144 <213> ORGANISM: Homo sapiens
146 <400> SEQUENCE: 12
147 Ala Asp Thr Gln Ala Leu Leu
148  1               5
151 <210> SEQ ID NO: 13
152 <211> LENGTH: 7
153 <212> TYPE: PRT
154 <213> ORGANISM: Saccharomyces cerevisiae
156 <400> SEQUENCE: 13
157 Asn Glu Gln Ser Pro Leu Leu
158  1               5
161 <210> SEQ ID NO: 14
162 <211> LENGTH: 12
163 <212> TYPE: PRT
164 <213> ORGANISM: Clostridium botulinum serotype A
166 <400> SEQUENCE: 14
167 Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp
168  1               5                   10
171 <210> SEQ ID NO: 15
172 <211> LENGTH: 11
173 <212> TYPE: PRT
174 <213> ORGANISM: Clostridium botulinum serotype A
176 <400> SEQUENCE: 15
177 Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp
178  1               5                   10
181 <210> SEQ ID NO: 16
182 <211> LENGTH: 4
183 <212> TYPE: PRT
184 <213> ORGANISM: Clostridium botulinum serotype A
186 <400> SEQUENCE: 16
187 Met Tyr Lys Asp
188  1
191 <210> SEQ ID NO: 17
192 <211> LENGTH: 7
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <221> NAME/KEY: SITE
198 <222> LOCATION: (1)...(7)
199 <223> OTHER INFORMATION: Consensus sequence for Leucine-based motif.
201 <221> NAME/KEY: VARIANT
202 <222> LOCATION: (1)...(1)
203 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 205 <221> VARIANT
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      206 <222> LOCATION: (3)...(5)
      207 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 209 <400> 17
W--> 210 Xaa Asp Xaa Xaa Xaa Leu Leu
      211  1               5
      214 <210> SEQ ID NO: 18
      215 <211> LENGTH: 7
      216 <212> TYPE: PRT
      217 <213> ORGANISM: Artificial Sequence
      219 <220> FEATURE:
      220 <221> NAME/KEY: SITE
      221 <222> LOCATION: (1)...(7)
      222 <223> OTHER INFORMATION: Consensus sequence for Leucine-based motif.
      224 <221> NAME/KEY: VARIANT
      225 <222> LOCATION: (1)...(1)
      226 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 228 <221> VARIANT
      229 <222> LOCATION: (3)...(5)
      230 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 232 <400> 18
W--> 233 Xaa Glu Xaa Xaa Xaa Leu Leu
      234  1               5
      237 <210> SEQ ID NO: 19
      238 <211> LENGTH: 7
      239 <212> TYPE: PRT
      240 <213> ORGANISM: Artificial Sequence
      242 <220> FEATURE:
      243 <221> NAME/KEY: SITE
      244 <222> LOCATION: (1)...(7)
      245 <223> OTHER INFORMATION: Consensus sequence for Leucine-based motif.
      247 <221> NAME/KEY: VARIANT
      248 <222> LOCATION: (1)...(1)
      249 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 251 <221> VARIANT
      252 <222> LOCATION: (3)...(5)
      253 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 255 <400> 19
W--> 256 Xaa Asp Xaa Xaa Xaa Leu Ile
      257  1               5
      260 <210> SEQ ID NO: 20
      261 <211> LENGTH: 7
      262 <212> TYPE: PRT
      263 <213> ORGANISM: Artificial Sequence
      265 <220> FEATURE:
      266 <221> NAME/KEY: SITE
      267 <222> LOCATION: (1)...(7)
      268 <223> OTHER INFORMATION: Consensus sequence for Leucine-based motif.
      270 <221> NAME/KEY: VARIANT
      271 <222> LOCATION: (1)...(1)
```

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       272 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 274 <221> VARIANT
       275 <222> LOCATION: (3)...(5)
       276 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 278 <400> 20
W--> 279 Xaa Asp Xaa Xaa Xaa Leu Met
       280  1                 5
       283 <210> SEQ ID NO: 21
       284 <211> LENGTH: 7
       285 <212> TYPE: PRT
       286 <213> ORGANISM: Artificial Sequence
       288 <220> FEATURE:
       289 <221> NAME/KEY: SITE
       290 <222> LOCATION: (1)...(7)
       291 <223> OTHER INFORMATION: Consensus sequence for Leucine-based motif.
       293 <221> NAME/KEY: VARIANT
       294 <222> LOCATION: (1)...(1)
       295 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 297 <221> VARIANT
       298 <222> LOCATION: (3)...(5)
       299 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 301 <400> 21
W--> 302 Xaa Glu Xaa Xaa Xaa Leu Ile
       303  1                 5
       306 <210> SEQ ID NO: 22
       307 <211> LENGTH: 7
       308 <212> TYPE: PRT
       309 <213> ORGANISM: Artificial Sequence
       311 <220> FEATURE:
       312 <221> NAME/KEY: SITE
       313 <222> LOCATION: (1)...(7)
       314 <223> OTHER INFORMATION: Consensus sequence for Leucine-based motif.
       316 <221> NAME/KEY: VARIANT
       317 <222> LOCATION: (1)...(1)
       318 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 320 <221> VARIANT
       321 <222> LOCATION: (3)...(5)
       322 <223> OTHER INFORMATION: Xaa is any amino acid.
W--> 324 <400> 22
W--> 325 Xaa Glu Xaa Xaa Xaa Ile Leu
       326  1                 5
       329 <210> SEQ ID NO: 23
       330 <211> LENGTH: 7
       331 <212> TYPE: PRT
       332 <213> ORGANISM: Artificial Sequence
       334 <220> FEATURE:
       335 <221> NAME/KEY: SITE
       336 <222> LOCATION: (1)...(7)
       337 <223> OTHER INFORMATION: Consensus sequence for Leucine-based motif.
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/05/2007
PATENT APPLICATION: US/10/757,077B   TIME: 14:53:28

Input Set : **A:\17355CIP3SEQLIST.TXT**
Output Set: **N:\CRF4\02052007\J757077B.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 1,3,4,5
Seq#:18; Xaa Pos. 1,3,4,5
Seq#:19; Xaa Pos. 1,3,4,5
Seq#:20; Xaa Pos. 1,3,4,5
Seq#:21; Xaa Pos. 1,3,4,5
Seq#:22; Xaa Pos. 1,3,4,5
Seq#:23; Xaa Pos. 1,3,4,5
Seq#:24; Xaa Pos. 2,3,4

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Input Set : **A:\17355CIP3SEQLIST.TXT**
Output Set: **N:\CRF4\02052007\J757077B.raw**

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L:205 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:209 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:228 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:232 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:251 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:255 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:274 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:278 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:297 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:301 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:320 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:324 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:343 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:347 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:366 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:370 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:905 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:53
L:926 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:54
L:951 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:55
L:972 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:56
L:976 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:56
L:1001 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:57
L:1022 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:58
L:1047 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:59
L:1068 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:60
L:1093 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:61
L:1114 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:62
L:1139 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:63
L:1143 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:63
L:1164 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:64
L:1189 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:65
L:1210 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:66
L:1235 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:67
L:1256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:68
L:1281 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:69
L:1285 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:69
L:1306 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:70
L:1331 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:71
L:1352 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:72
L:1377 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:73
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VERIFICATION SUMMARY   DATE: 02/05/2007
PATENT APPLICATION: **US/10/757,077B**   TIME: 14:53:28

Input Set : **A:\17355CIP3SEQLIST.TXT**
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L:1398 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:74
L:1402 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:74
L:1427 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:75
L:1448 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:76
L:1473 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:77
L:1494 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:78
L:1519 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:79
L:1540 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:80
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